

# *Lactobacillus* Genomics and Metabolic Engineering

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Cover design adapted from images provided by Sandra M. Ruza: scanning electron microscopy images of *Lactobacillus acidophilus* grown with and without high salt.

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# Preface

The *Lactobacillus* genus comprises more than 200 formally recognized species characterized by their phylogenetic and metabolic diversity. Lactobacilli species are found in a variety of ecological niches such as decomposing plant materials, wine, meat and raw milk and are often commensals to plants and animals including humans. They are food-grade microorganisms widely applied in the fermented food industry due to their technological and health-promoting properties; these bacteria have been extensively used as starter cultures and as probiotics. This ten-chapter book aims to survey the most relevant aspects of the genus. Due to the available genomic information for the *Lactobacillus* genus, comparative genomic approaches have been taken to evaluate strains or species found in different niches, to give an insight into niche adaptation within the genus (see Chapters 1 and 2). A detailed description of the catabolic pathways of complex carbohydrates metabolism (see Chapter 3) and their relation to their main fermentation product, lactic acid (see Chapter 4) are depicted; the ability of *Lactobacillus* to respond to environmental conditions, focusing on osmotic

stress, by altering the nature of their cell wall for adaptation are explored (see Chapter 5). In particular, focus is made on S-layer proteins, with relevant and updated concepts regarding genetics, structural features, cell wall and self-assembly, functionality and biotechnological applications (see Chapter 6). Also, an updated revision is presented of phages infecting strains of *Lactobacillus* spp. with particular emphasis on structural studies on phage–host interactions (see Chapter 7). Overview of methods for the introduction of DNA into *Lactobacillus* species are described (see Chapter 8) and also tools and applications in different areas for recombinant gene expression (see Chapter 9). Finally, since commensal and environmental bacteria appear as a reservoir of antibiotic resistance genes, a genomic overview of these resistance genes in *Lactobacillus* are described (see Chapter 10).

I would like to express my gratitude to all the authors for their hard work and effort in contributing to this book. I am also very grateful to Annette Griffin at Caister Academic Press, who invited me to edit this book.

Sandra M. Ruzal

